

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 27, 2005, 19:39:12 ; Search time 142 Seconds
(without alignments)
27.987 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKXAEED 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 252723

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	51.9	13	14	US-10-199-869-23
2	26	48.1	13	15	US-10-308-128-29
3	26	48.1	15	14	US-10-210-428-25
4	26	48.1	15	17	US-10-862-074-25
5	25	46.3	12	14	US-10-084-813-925
6	25	46.3	12	14	US-10-084-813-926
7	25	46.3	14	9	US-09-999-699-7
8	25	46.3	15	14	US-10-084-813-689
9	25	46.3	15	14	US-10-084-813-690
10	25	46.3	15	14	US-10-084-813-691
11	25	46.3	15	14	US-10-084-813-692
12	25	46.3	15	14	US-10-084-813-693
13	24	44.4	14	17	US-10-474-298-19

14	24	44.4	14	17	US-10-474-298-23	Sequence 23, Appl
15	23	42.6	6	17	US-10-654-578-1897	Sequence 1897, Ap
16	23	42.6	10	14	US-10-190-082-380	Sequence 380, App
17	23	42.6	12	9	US-09-848-664-5	Sequence 5, Appl
18	23	42.6	12	14	US-10-190-082-387	Sequence 387, App
19	23	42.6	12	16	US-10-652-407-58	Sequence 58, Appl
20	23	42.6	13	10	US-09-201-396-2	Sequence 2, Appl
21	23	42.6	13	10	US-09-965-364-37	Sequence 37, Appl
22	23	42.6	13	14	US-10-277-607-2	Sequence 2, Appl
23	23	42.6	14	17	US-10-865-478-847	Sequence 847, App
24	23	42.6	15	14	US-10-221-894-34	Sequence 34, Appl
25	23	42.6	15	14	US-10-221-889-34	Sequence 34, Appl
26	23	42.6	15	15	US-10-224-268-3	Sequence 3, Appl
27	23	42.6	15	15	US-10-644-703-6	Sequence 6, Appl
28	23	42.6	15	17	US-10-641-633-52	Sequence 52, Appl
29	22	40.7	6	14	US-10-106-804B-14	Sequence 14, Appl
30	22	40.7	6	14	US-10-323-046-16	Sequence 16, Appl
31	22	40.7	6	17	US-10-654-578-1564	Sequence 1564, Ap
32	22	40.7	7	14	US-10-006-869-3417	Sequence 3417, Ap
33	22	40.7	7	14	US-10-006-869-3432	Sequence 3432, Ap
34	22	40.7	7	14	US-10-006-869-3501	Sequence 3501, Ap
35	22	40.7	7	14	US-10-006-869-3516	Sequence 3516, Ap
36	22	40.7	7	14	US-10-190-082-644	Sequence 644, App
37	22	40.7	7	14	US-10-395-032-3417	Sequence 3417, Ap
38	22	40.7	7	14	US-10-395-032-3432	Sequence 3432, Ap
39	22	40.7	7	14	US-10-395-032-3501	Sequence 3501, Ap
40	22	40.7	7	14	US-10-395-032-3516	Sequence 3516, Ap
41	22	40.7	7	17	US-10-654-578-761	Sequence 761, App
42	22	40.7	7	17	US-10-654-578-776	Sequence 776, App
43	22	40.7	7	17	US-10-654-578-845	Sequence 845, App
44	22	40.7	7	17	US-10-654-578-860	Sequence 860, App
45	22	40.7	8	14	US-10-006-869-3418	Sequence 3418, Ap
46	22	40.7	8	14	US-10-006-869-3433	Sequence 3433, Ap
47	22	40.7	8	14	US-10-006-869-3502	Sequence 3502, Ap
48	22	40.7	8	14	US-10-006-869-3517	Sequence 3517, Ap
49	22	40.7	8	14	US-10-395-032-3418	Sequence 3418, Ap
50	22	40.7	8	14	US-10-395-032-3433	Sequence 3433, Ap

ALIGNMENTS

RESULT 1
US-10-199-869-23
; Sequence 23, Application US/10199869
; Publication No. US20030152953A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SU
; FILE REFERENCE: D0161 NP
; CURRENT APPLICATION NUMBER: US/10/199,869
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/306,577
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-869-23
Query Match 51.9%; Score 28; DB 14; Length 13;
Best local similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 4 FRSRLKXAEED 12
FRSRLKXAEED 10
FRSRLKXAEED 12

RESULT 2

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OM protein - protein search, using SW model

Run on: January 27, 2005, 19:30:31 ; Search time 38 seconds
(without alignments)
19.197 Million cell updates/sec

Title: US-09-830-837a-77

Perfect score: 54

Sequence: 1 VFRSLKXAEED 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

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1: Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	25	46.3	14	2 US-08-883-070-4	Sequence 4, Appl
5	25	46.3	14	4 US-09-999-699-7	Sequence 7, Appl
6	23	42.6	6	4 US-09-535-852-1897	Sequence 1897, Ap
7	23	42.6	7	1 US-08-082-847-17	Sequence 17, Appl
8	23	42.6	8	1 US-08-082-847-7	Sequence 7, Appl
9	23	42.6	8	1 US-08-082-847-9	Sequence 9, Appl
10	23	42.6	8	1 US-08-082-847-29	Sequence 29, Appl
11	23	42.6	8	4 US-09-680-571A-84	Sequence 84, Appl
12	23	42.6	8	4 US-09-680-571A-86	Sequence 86, Appl
13	23	42.6	9	1 US-08-082-847-31	Sequence 31, Appl
14	23	42.6	9	1 US-08-082-847-32	Sequence 32, Appl
15	23	42.6	9	1 US-08-082-847-35	Sequence 35, Appl
16	23	42.6	9	1 US-08-082-847-36	Sequence 36, Appl
17	23	42.6	10	1 US-07-830-330-13	Sequence 13, Appl
18	23	42.6	10	1 US-08-082-847-19	Sequence 19, Appl
19	23	42.6	10	1 US-08-082-847-21	Sequence 21, Appl
20	23	42.6	10	1 US-08-133-271-6	Sequence 6, Appl
21	23	42.6	10	3 US-08-855-958-1	Sequence 1, Appl
22	23	42.6	10	3 US-08-855-958-7	Sequence 7, Appl
23	23	42.6	10	3 US-08-855-958-8	Sequence 8, Appl
24	23	42.6	11	3 US-08-855-958-4	Sequence 4, Appl
25	23	42.6	11	3 US-08-855-958-9	Sequence 9, Appl
26	23	42.6	12	4 US-09-848-664A-5	Sequence 5, Appl
27	23	42.6	13	1 US-07-830-330-14	Sequence 14, Appl

28	23	42.6	15	1 US-07-830-330-15	Sequence 15, Appl
29	23	42.6	15	1 US-08-133-271-1	Sequence 1, Appl
30	23	42.6	15	3 US-09-045-632-105	Sequence 105, App
31	23	42.6	15	3 US-08-855-958-5	Sequence 5, Appl
32	22	40.7	6	1 US-08-082-847-4	Sequence 4, Appl
33	22	40.7	6	1 US-08-393-305-15	Sequence 15, Appl
34	22	40.7	6	1 US-08-726-817-15	Sequence 15, Appl
35	22	40.7	6	2 US-08-725-969-15	Sequence 15, Appl
36	22	40.7	6	2 US-08-794-524-15	Sequence 15, Appl
37	22	40.7	6	3 US-09-189-193-15	Sequence 15, Appl
38	22	40.7	6	3 US-09-360-237-41	Sequence 41, Appl
39	22	40.7	6	4 US-09-675-922-16	Sequence 16, Appl
40	22	40.7	6	4 US-09-535-852-1564	Sequence 1564, Ap
41	22	40.7	7	1 US-08-082-847-15	Sequence 15, Appl
42	22	40.7	7	1 US-08-082-847-16	Sequence 16, Appl
43	22	40.7	7	1 US-08-082-847-18	Sequence 18, Appl
44	22	40.7	7	3 US-09-360-237-32	Sequence 32, Appl
45	22	40.7	7	3 US-09-187-859-3417	Sequence 3417, Ap
46	22	40.7	7	3 US-09-187-859-3432	Sequence 3432, Ap
47	22	40.7	7	3 US-09-187-859-3501	Sequence 3501, Ap
48	22	40.7	7	3 US-09-187-859-3516	Sequence 3516, Ap
49	22	40.7	7	4 US-09-839-542B-3417	Sequence 3417, Ap
50	22	40.7	7	4 US-09-839-542B-3432	Sequence 3432, Ap

ALIGNMENTS

```

RESULT 1
US-09-360-237-13
; Sequence 13, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAMSON, ROBERT B.
; APPLICANT: SAKAI, JUNO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-13

Query Match      51.9%; Score 28; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VFRSLK 6
Db      1 VFRSLK 6

RESULT 2
US-09-360-237-14
; Sequence 14, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG

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OM protein - protein search, using SW model

Run on: January 27, 2005, 19:22:45 ; Search time 39 Seconds
(without alignments)
27.138 Million cell updates/sec

Title: US-09-830-837A-77
Perfect score: 54
Sequence: 1 VFRSLKTYAESD 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	35.2	10	2 JCI367	thyroliberin poten
3	19	35.2	11	2 A26930	emrg leader peptid
4	18	33.3	9	2 P60253	glycine cleavage s
5	18	33.3	10	2 P70322	ig heavy chain CRD
6	18	33.3	11	2 PC2372	58k heat shock pro
7	18	33.3	11	2 B29806	acidic proline-ric
8	18	33.3	15	2 PA0093	emiatin synthetas
9	18	33.3	15	2 B45133	casein kinase II (
10	17	31.5	11	2 I54193	Rhesus blood group
11	17	31.5	12	2 PH1611	ig H chain V-D-J r
12	17	31.5	15	2 JN0730	hypothetical 1.7K
13	16	29.6	7	2 S17976	glucose isomerase
14	16	29.6	8	2 S45651	probable Na+-trans
15	16	29.6	8	2 S37141	tpa protein - Brw
16	16	29.6	9	2 A44873	caldesmon - rabbit
17	16	29.6	9	2 P70324	ig heavy chain CRD
18	16	29.6	9	2 S02384	probable membrane
19	16	29.6	9	2 PC2073	ubiquinol-cytochro
20	16	29.6	10	2 S77990	cytochrome-c oxida
21	16	29.6	11	2 PH0914	T-cell receptor be
22	16	29.6	12	2 PH0936	T-cell receptor be
23	16	29.6	13	2 P70290	ig heavy chain CRD
24	16	29.6	13	2 H56046	urinary tract acron
25	16	29.6	14	1 LFECPS	phST operon leade
26	16	29.6	14	2 F90931	phST operon leade
27	16	29.6	14	2 B85780	phST operon leade
28	16	29.6	14	2 I64815	carbonic anhydrase
29	16	29.6	14	2 AG0705	phenylalanyl-tRNA

30	16	29.6	14	2 AF0296	phenylalanyl-tRNA
31	16	29.6	15	2 PA0086	protein QP200044 -
32	16	29.6	15	2 PA0099	phenotypic variati
33	16	29.6	15	2 PA0059	protein QP200021 -
34	16	29.6	15	2 S04586	NADH2 dehydrogenas
35	15	27.8	10	2 S65728	hemoglobin, extrac
36	15	27.8	10	2 A44871	monodehydroascorba
37	15	27.8	10	2 GAH01	gastric juice pept
38	15	27.8	11	2 S66606	quinoline 2-oxidor
39	15	27.8	12	2 P00730	unidentified 5.4/3
40	15	27.8	13	2 S41209	P470-non-reducing-
41	15	27.8	13	2 S60396	antigen 788/2 - ma
42	15	27.8	13	2 I54984	aeg-46.5 protein -
43	15	27.8	14	2 I54284	Cl-inhibitor - hum
44	15	27.8	14	2 B28018	very late antigen-
45	15	27.8	14	2 I49514	B144 protein A - m
46	15	27.8	14	2 PC4376	telomeric and tetr
47	15	27.8	14	2 S68095	calcium-binding pr
48	15	27.8	15	2 A60834	angiotensin I prec
49	15	27.8	15	2 S13973	chlorophyll a/b-bi
50	15	27.8	15	2 S62620	protein disulfide-

ALIGNMENTS

RESULT 1
PA0036
glycine cleavage system protein H1 and H2 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PA0036
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.
submitted to JRPD, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimension
A:Reference number: PA0001
A:Accession: PA0036
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Cross-references: UNIPROT:Q7M1X0
A:Experimental source: stem

Query Match 44.4%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 VFRSLKTYA 8
DB 3 VLEGKTYA 10

RESULT 2
JCI367
thyroliberin potentiating neuropeptide - bovine
N:Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI367
R:Butant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolae, P.
Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992
A>Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine
A:Reference number: JCI367; MUID:93111999; PMID:1472021
A:Accession: JCI367
A:Molecule type: protein
A:Residues: 1-10 <BDU>
A:Cross-references: UNIPROT:Q7M2Z8
A:Experimental source: hypothalamus
C:Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor
C:Function: A:Description: potentiates thyroliberin-induced thyrotropin secretion
C:Superfamily: thyroliberin
C:Keywords: hypothalamus; neuropeptide

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OM protein - protein search, using sw model

Run on: January 27, 2005, 19:21:20 ; Search time 156 Seconds

(without alignments)
25,295 Million cell updates/sec

Title: US-09-830-837a-77

Sequence: 1 VFRSLKYAESD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_23sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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3	54	100.0	14 3 AAB06329	AAB06329 Synthetic
4	54	100.0	15 3 AAB06325	AAB06325 Human sub
5	54	100.0	15 3 AAB06289	AAB06289 Synthetic
6	44	81.5	12 3 AAB06330	AAB06330 Synthetic
7	28	51.9	6 4 AAB97409	AAB97409 Peptide s
8	28	51.9	6 4 AAB97409	AAB97409 Site-1 pr
9	28	51.9	6 4 AAB97420	AAB97420 Site-1 pr
10	28	51.9	8 3 AAB06285	AAB06285 Human SKI
11	28	51.9	8 3 AAB84230	AAB84230 Amilo aci
12	28	51.9	8 3 AAB97403	AAB97403 Peptide s
13	28	51.9	13 4 AAB97403	AAB97403 Site-1 pr
14	28	51.9	13 4 AAB97403	AAB97403 Site-1 pr
15	27	50.0	12 4 AAB98241	AAB98241 Human pot
16	27	50.0	15 4 AAB64901	AAB64901 Human kin
17	26	48.1	9 6 ABR13967	ABR13967 Human can
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21	26	48.1	9 6 ABR13662	ABR13662 Human can
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23	26	48.1	10 3 AAB75671	AAB75671 HLA class
24	26	48.1	10 6 ABR14084	ABR14084 Human can
25	26	48.1	10 6 ABR13509	ABR13509 Human can

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32	26	48.1	10 6 ABR13151	ABR13151 Human can
33	26	48.1	13 7 AAY18293	AAY18293 Tendamiat
34	26	48.1	15 6 AAY18294	AAY18294 Tendamiat
35	26	48.1	15 6 ABR33503	ABR33503 Human can
36	26	48.1	15 6 ABR33235	ABR33235 Human can
37	26	48.1	15 6 ABR33183	ABR33183 Human can
38	26	48.1	15 6 ABR33565	ABR33565 Human can
39	26	48.1	15 6 ABR33182	ABR33182 Human can
40	26	48.1	15 6 ABR33209	ABR33209 Human can
41	26	48.1	15 6 ABR71611	ABR71611 HSV-1 pep
42	26	48.1	7 8 ADN08728	ADN08728 Cotton wI
43	25	46.3	9 2 AAR37434	AAR37434 Promega P
44	25	46.3	9 2 AAW09657	AAW09657 Labelled
45	25	46.3	10 4 AAG70027	AAG70027 Backbone
46	25	46.3	11 4 AAG68683	AAG68683 Human Chk
47	25	46.3	11 4 AAB89819	AAB89819 HIV gp120
48	25	46.3	12 4 AAB89818	AAB89818 HIV gp120
49	25	46.3		
50	25	46.3		

ALIGNMENTS

RESULT 1
AAB06265 standard; peptide: 11 AA.
ID AAB06265
XX
AC AAB06265;
XX
DT 03-OCT-2000 (first entry)
XX
DE Subtilisin-kexin SK-1 peptide substrate #1.
XX
KW Subtilisin-kexin isoenzyme 1; SKI-1; antilipase; cytosolic;
KW vasotrophic; SKI-1 inhibitor; hypercholesterolemia; liver steatosis;
KW Ras-dependent cancer; restenosis; amyloid protein formation;
KW pro-brain-derived neurotrophic factor; proBDNF.
XX
OS Synthetic.
XX
PN WO200026348-A2.
XX
PD 11-MAY-2000.
XX
PP 04-NOV-1999; 99WO-CAB01058.
XX
PR 04-NOV-1998; 98CA-02249648.
XX
PA (RECU-) INST RECH CLINIQUES MONTREAL.
XX
PI Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;
XX WPI; 2000-365601/31.
XX
DR Novel soluble proteic fragment of subtilisin-kexin isoenzyme for
XX producing a polypeptide useful for treating hypercholesterolemia, liver
XX steatosis and amyloidosis, comprises a specific amino acid sequence.
XX
PS Claim 26; Page 83; 119pp; English.
XX
CC The present sequence is a peptide which is capable of binding to and of
CC being cleaved by the subtilisin-kexin isoenzyme 1 (SKI-1) catalytic site.
CC SKI-1 is a type-I membrane-bound proteinase which is highly conserved in
CC humans, mice and rats. SKI-1 cleaves at a specific threonine residue
CC within the N-terminal segment of human pro-brain-derived neurotrophic
CC factor (proBDNF). The present peptide may be used for monitoring SKI-1

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OM protein - protein search, using sw model

Run on: August 17, 2005, 15:36:20 ; Search time 169 Seconds

(without alignment)
2400.492 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052

Perfect score: 5537
Sequence: 1 GKRLGDRLEKKSFEKAPCP.....PRVKRPMQVHPKPTSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5537	100.0	1052	9 US-09-060-854B-7	Sequence 7, Appl1
2	5537	100.0	1052	9 US-09-891-711-4	Sequence 4, Appl1
3	5537	100.0	1052	15 US-10-665-689-6	Sequence 6, Appl1
4	5537	100.0	1052	16 US-10-829-118-4	Sequence 4, Appl1
5	5537	100.0	1052	18 US-10-924-092A-208	Sequence 208, App
6	5537	100.0	1052	20 US-11-020-628-208	Sequence 208, App
7	5408	97.7	1052	9 US-09-891-711-6	Sequence 6, Appl1
8	5408	97.7	1052	16 US-10-829-118-6	Sequence 6, Appl1
9	3549	64.1	666	15 US-10-264-237-2631	Sequence 2631, Ap
10	2428	43.9	497	15 US-10-104-047-2347	Sequence 2347, Ap
11	1768.5	31.9	663	15 US-10-424-599-255271	Sequence 255271,

12	1664	30.1	2605	16 US-10-437-963-138449	Sequence 138449,
13	1467	26.5	280	18 US-10-924-092A-209	Sequence 209, App
14	1467	26.5	280	20 US-11-020-628-209	Sequence 209, App
15	663	12.0	224	16 US-10-767-701-55268	Sequence 55268, A
16	526	9.5	315	15 US-10-424-599-255270	Sequence 255270,
17	340	6.1	315	15 US-10-424-599-222557	Sequence 222557,
18	338.5	6.1	381	16 US-10-647-131-3	Sequence 3, Appl1
19	338.5	6.1	381	16 US-10-647-131-4	Sequence 4, Appl1
20	337.5	6.1	357	9 US-09-837-235-15	Sequence 15, Appl
21	337.5	6.1	357	20 US-11-043-731-15	Sequence 15, Appl
22	337.5	6.1	1139	14 US-10-156-761-10856	Sequence 10856, A
23	336.5	6.1	1079	14 US-10-112-488-39	Sequence 39, Appl
24	336.5	6.1	1079	16 US-10-673-860-8	Sequence 8, Appl1
25	333.5	6.0	379	10 US-09-813-408-11	Sequence 11, Appl
26	333.5	6.0	381	16 US-10-647-131-2	Sequence 11, Appl
27	332.5	6.0	381	9 US-09-920-118-16	Sequence 16, Appl
28	331.5	6.0	379	9 US-09-920-118-14	Sequence 14, Appl
29	329	5.9	379	10 US-09-813-408-10	Sequence 10, Appl
30	329	5.9	379	15 US-10-146-905A-10	Sequence 10, Appl
31	329	5.9	380	15 US-10-146-905A-12	Sequence 12, Appl
32	326.5	5.9	275	14 US-10-324-152-22	Sequence 22, Appl
33	325	5.9	380	10 US-09-813-408-16	Sequence 16, Appl
34	324.5	5.9	275	14 US-10-324-152-6	Sequence 6, Appl1
35	324.5	5.9	275	14 US-10-324-152-11	Sequence 11, Appl
36	324.5	5.9	275	17 US-10-872-166-14	Sequence 14, Appl
37	324.5	5.9	275	17 US-10-872-166-15	Sequence 15, Appl
38	324.5	5.9	275	17 US-10-873-917-11	Sequence 11, Appl
39	324.5	5.9	275	17 US-10-873-610-16	Sequence 16, Appl
40	324.5	5.9	275	17 US-10-872-162-11	Sequence 11, Appl
41	324.5	5.9	275	17 US-10-872-162-13	Sequence 13, Appl
42	324.5	5.9	276	17 US-10-873-917-14	Sequence 14, Appl
43	324	5.9	276	17 US-10-873-917-13	Sequence 13, Appl
44	323.5	5.8	275	8 US-08-322-678-8	Sequence 8, Appl1
45	323.5	5.8	275	9 US-09-060-854B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-060-854B-7
Sequence 7, Application US/09060854B
Patent No. US20020081703A1
GENERAL INFORMATION:
APPLICANT: Esce11, David Aaron
TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. US20020081703A1
FILE REFERENCE: GCS32
CURRENT APPLICATION NUMBER: US/09/060,854B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1052
TYPE: PRT
ORGANISM: Homo sapien
US-09-060-854B-7

Query Match	100.0%	Score 5537	DB 9	Length 1052
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1036	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	1	GKRLGDRLEKKSFEKAPCPGCSHLLTVKVRSSVTVYEVYVAFNGYTPAKRNSPISA	60	
DB	17	GKRLGDRLEKKSFEKAPCPGCSHLLTVKVRSSVTVYEVYVAFNGYTPAKRNSPISA	76	
QY	61	LKSSVDNRRLIPRNPSPDPSDEYVQIEKQAGLLTLEDHNIKRVTPQRYFSL	120	
DB	77	LKSSVDNRRLIPRNPSPDPSDEYVQIEKQAGLLTLEDHNIKRVTPQRYFSL	136	
QY	121	KYASDPTVPCNETRWGQKQSSRPLRPAISLSGFWHATGRSSRLIRAIPOVAQT	180	

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OM protein - protein search, using BW model

Run on: August 17, 2005, 15:32:39 ; Search time 44 Seconds
(without alignments)
1757.646 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKHLGRLKESFEKAPCP.....PRVKRPQLMQVHPKTPSV 1036

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTOS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5537	100.0	1052	3	US-09-360-237-3
3	5537	100.0	1052	4	US-09-255-501-208
4	5537	100.0	1052	4	US-09-060-854B-7
5	5537	100.0	1052	4	US-09-891-711-4
6	5537	100.0	1052	4	US-09-949-016-6413
7	5537	100.0	1052	4	US-09-060-872A-208
8	5537	100.0	1052	4	US-09-500-135C-208
9	5537	100.0	1058	4	US-09-949-016-10687
10	5408	97.7	1052	3	US-09-360-237-1
11	5408	97.7	1052	4	US-09-891-711-6
12	1467	26.5	280	4	US-09-255-501-209
13	1467	26.5	280	4	US-09-060-872A-209
14	1467	26.5	280	4	US-09-500-135C-209
15	372.5	6.7	176	4	US-09-270-767-31702
16	338.5	6.1	352	1	US-07-923-260A-6
17	337.5	6.1	352	1	US-07-923-260A-1
18	337.5	6.1	381	1	US-07-772-087-5
19	337.5	6.1	381	1	US-08-322-965-2
20	330.5	6.0	275	1	US-07-864-298-1
21	329	5.9	350	1	US-07-923-260A-4
22	329	5.9	379	2	US-08-845-295A-1
23	329	5.9	379	3	US-09-140-933-1
24	329	5.9	379	3	US-09-146-661-1
25	329	5.9	379	3	US-09-150-515-1
26	327	5.9	378	1	US-07-772-087-4
27	323.5	5.8	275	1	US-08-322-677A-8

28	323.5	5.8	275	1	US-08-322-676-8	Sequence 8, Appl1
29	323.5	5.8	275	3	US-08-898-218-8	Sequence 8, Appl1
30	323.5	5.8	275	3	US-08-848-793-8	Sequence 8, Appl1
31	323.5	5.8	275	3	US-09-255-502-3	Sequence 3, Appl1
32	323.5	5.8	275	3	US-09-178-155-4	Sequence 3, Appl1
33	323.5	5.8	275	3	US-09-445-270-3	Sequence 3, Appl1
34	323.5	5.8	275	4	US-09-178-173A-4	Sequence 4, Appl1
35	323.5	5.8	275	4	US-08-322-678-8	Sequence 8, Appl1
36	323.5	5.8	275	4	US-09-255-501-4	Sequence 4, Appl1
37	323.5	5.8	275	4	US-09-060-854B-4	Sequence 4, Appl1
38	323.5	5.8	275	4	US-09-177-353-4	Sequence 4, Appl1
39	323.5	5.8	275	4	US-10-033-325-4	Sequence 4, Appl1
40	323.5	5.8	275	4	US-09-529-904-5	Sequence 5, Appl1
41	323.5	5.8	275	4	US-09-060-872A-4	Sequence 4, Appl1
42	323.5	5.8	275	4	US-09-500-135C-4	Sequence 4, Appl1
43	323.5	5.8	275	6	5472855-4	Sequence 4, Appl1
44	323.5	5.8	275	6	5472855-4	Sequence 4, Appl1
45	323.5	5.8	352	1	US-07-923-260A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1									
US-09-255-502-7									
; Sequence 7, Application US/09255502									
; Patent No. 6218165									
; GENERAL INFORMATION:									
; APPLICANT: Bateil, David									
; TITLE OF INVENTION: Mutant Proteins Having Lower Allergic Responses in									
; TITLE OF INVENTION: Humans and Methods for Constructing, Identifying and									
; TITLE OF INVENTION: Producing Such Proteins									
; FILE REFERENCES: GC 527-D2									
; CURRENT APPLICATION NUMBER: US/09/255,502									
; PRIOR FILING DATE: 1999-02-23									
; PRIOR APPLICATION NUMBER: 09/060,872									
; PRIOR FILING DATE: 1998-04-15									
; NUMBER OF SEQ ID NOS: 7									
; SOFTWARE: Patentin Ver. 2.0									
; SEQ ID NO 7									
; LENGTH: 1052									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-255-502-7									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	17	GKHLGRLKESFEKAPCPGCSHLTKVERFSSTVEYEVIAENGFTAKARNSFISSA	76						
QY	61	LKSEVUNNMIIIPNNSSSDYPSDFEYIOTKCKAGLTLLEDPNIRKTVPOKVRPSL	120						
DB	77	LKSEVUNNMIIIPNNSSSDYPSDFEYIOTKCKAGLTLLEDPNIRKTVPOKVRPSL	136						
QY	121	KYASDPVTCNETRMSQKMSRPLRARSISLGSFWMHATGRSSRLRAIPROVAQT	180						
DB	137	KYASDPVTCNETRMSQKMSRPLRARSISLGSFWMHATGRSSRLRAIPROVAQT	196						
QY	181	LOADVLMQMGYTGANVAVFDGLSEKHPKPNXKERTWTNERTLDDGIGHGTFVAGV	240						
DB	197	LOADVLMQMGYTGANVAVFDGLSEKHPKPNXKERTWTNERTLDDGIGHGTFVAGV	256						
QY	241	IASRECOGAPPAELHIFRFTNNQVSYTSWFLDAENVAILKKIDVLANSTIGPDDMDH	300						
DB	257	IASRECOGAPPAELHIFRFTNNQVSYTSWFLDAENVAILKKIDVLANSTIGPDDMDH	316						
QY	301	PFVDKVELTANNVIMVSAIGNDGPLYGTLANPADQMDVGVGGIDPEDNIARSSRGMT	360						
DB	317	PFVDKVELTANNVIMVSAIGNDGPLYGTLANPADQMDVGVGGIDPEDNIARSSRGMT	376						

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OM protein - protein search, using bw model

Run on: August 17, 2005, 15:31:04 ; Search time 183 Seconds

(without alignments)
2898.984 Million cell updates/sec

Title: US-09-830-837a-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKXHLGDRLEKKSFEKAPCP.....PRVKRPQLMQVHPKTPSV 1036

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5537	100.0	1052	1 MSIP_HUMAN	Q14703 homo sapien
2	5408	97.7	1052	1 MSIP_CRICR	Q92268 cricetus
3	5396	97.5	1052	1 MSIP_RAT	Q9W223 ratu
4	5360	96.8	1052	1 MSIP_MOUSE	Q9W222 mus musculu
5	5357	96.7	1052	2 O6PG67	Q9W222 mus musculu
6	5339	96.4	1055	2 O80U80	Q80U80 mus musculu
7	4770	86.1	1074	2 O6X1U1	Q6X1U1 brachydanio
8	4522	81.7	950	2 O6AX98	Q6AX98 xenopus lae
9	2835	51.2	952	2 O8TAN4	Q8TAN4 homo sapien
10	2815.5	50.8	1238	2 O7PVB0	Q7PVB0 anopheles g
11	2377.5	42.9	1012	2 O9VPI0	Q9VPI0 drosophila
12	2269	41.0	1038	2 O8L7B7	Q8L7B7 arabidopsis
13	355	6.4	1239	2 O9F8Z4	Q9F8Z4 streptomyce
14	346.5	6.3	1722	2 O9NDZ2	Q9NDZ2 leishmania
15	339.5	6.1	1381	2 O84F18	Q84F18 bacillus su
16	338.5	6.1	381	1 SUBN_BACNA	P35835 bacillus su
17	338.5	6.1	381	1 SUBT_BACSA	P00783 bacillus su
18	338.5	6.1	381	1 SUBT_BACST	P29147 bacillus st
19	337.5	6.1	381	1 SUBT_BACSU	P4188 bacillus su
20	337.5	6.1	1139	2 O82139	Q82139 streptomyce
21	336	6.1	1102	2 O9R564	P95684 streptomyce
22	335.5	6.0	1245	2 O9R564	Q9R564 streptomyce
23	333.5	6.0	379	2 O9FDP4	Q9FDP4 bacillus li
24	333.5	6.0	379	2 O65LP7	Q65LP7 bacillus li
25	333.5	6.0	381	2 O847A2	Q847A2 bacillus su
26	329	5.9	379	1 SUBT_BACLI	P0780 bacillus li
27	327.5	5.8	627	1 O9RUD0	Q9RUD0 deino
28	322	5.8	382	2 O45522	Q45522 bacillus sp
29	321	5.8	379	2 O45301	Q45301 bacillus li
30	321	5.8	379	2 O6BCN9	Q6BCN9 bacillus mo
31	321	5.8	379	2 O6PNNS	Q6PNNS bacillus li

32	320.5	5.8	275	2	O93166	O93166 bacillus su
33	320.5	5.8	379	2	O45300	O45300 bacillus li
34	320	5.8	1105	2	O8KX16	O8KX16 streptomyce
35	318.5	5.8	374	2	O9F942	O9F942 bacillus li
36	318.5	5.8	381	2	O7WVA6	O7WVA6 bacillus su
37	318.5	5.8	382	1	SUBT_BACAM	P00786 bacillus am
38	318	5.7	374	2	O9F943	O9F943 bacillus li
39	317	5.7	379	2	O53521	O53521 bacillus li
40	316.5	5.7	275	1	SUBT_BACPU	P07518 bacillus pu
41	316.5	5.7	382	2	O6IT79	O6IT79 bacillus sp
42	316	5.7	374	2	O9F941	O9F941 bacillus li
43	314.5	5.7	312	2	O93020	O93020 clostridium
44	314	5.7	404	2	O76129	O76129 bacillus sp
45	314	5.7	1237	2	O8GCT4	O8GCT4 streptomyce

ALIGNMENTS

RESULT 1
MSIP_HUMAN STANDARD; PRT; 1052 AA.
ID MSIP_HUMAN
AC Q14703; Q9UF67;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Membrane-bound transcription factor site-1 protease precursor
DB (EC 3.4.21.-) (Site-1 protease) (Subtilisin/kexin-isozyme-1) (SKI-1).
GN Name=MBTSP1; Synonyms=KIAA0091, SIP, SKI1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid;
RX MEDLINE=20401147; PubMed=10944850;
RA Nakajima T., Iwaki K., Kodama T., Inazawa J., Emi M.;
RT "Genomic structure and chromosomal mapping of the human site-1
RT protease (SIP) gene.";
RT J. Hum. Genet. 45:212-217(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. III.
RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RT DNA Res. 2:37-43(1995).
RN [3]
RP SEQUENCE OF 735-1052 FROM N.A.
RC TISSUE=Testis;
RX Submitted (DCC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION, PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=20112799; PubMed=10644685; DOI=10.1074/jbc.275.4.2349;
RA Toure B.B., Munzer J.S., Basak A., Benjannet S., Rochemont J.,
RA Lazure C., Chretien M., Seidah N.G.;
RT "Biosynthesis and enzymatic characterization of human SKI-1/SIP and
RT the processing of its inhibitory prosegment.";
RT J. Biol. Chem. 275:2349-2358(2000).
RN [5]
RP SUBCELLULAR LOCATION.
RX MEDLINE=9915548; PubMed=9990022; DOI=10.1073/pnas.96.4.1321;
RA Toure B.B., Basak A., Munzer J.S., Marcinkiewicz J., Zhong M.,
RA Barale J.-C., Lazure C., Murphy R.A., Chretien M., Marcinkiewicz M.;
RT "Mammalian subtilisin/kexin isozyyme SKI-1: a widely expressed
RT proprotein convertase with a unique cleavage specificity and cellular
RT localization.";

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OM protein - protein search, using sw model

Run on: August 17, 2005, 15:19:31 ; Search time 48 Seconds
(without alignments)
2076.678 Million cell updates/sec

Title: US-09-830-837a-6_COPY_17_1052
Perfect score: 5537
Sequence: 1 GKXHLGDRLEKKSFEKAPCP.....PRVRRPOLMQGVHPKTPSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5408	97.7	1052	2 T17093	intraluminal subti
2	1716	31.0	318	2 T43492	hypothetical prote
3	338.5	6.1	381	1 SUBSS	subtilisin (EC 3.4
4	338.5	6.1	381	2 JQ1487	subtilisin (EC 3.4
5	338.5	6.1	381	2 JH0778	subtilisin (EC 3.4
6	337.5	6.1	381	1 SUBSI	subtilisin (EC 3.4
7	329	5.9	379	1 SUBSC	subtilisin (EC 3.4
8	327.5	5.9	379	2 D75393	serine proteinase,
9	322	5.8	382	2 I39780	subtilisin (EC 3.4
10	318.5	5.8	382	1 SUBSN	subtilisin (EC 3.4
11	312.5	5.6	272	2 A23624	subtilisin (EC 3.4
12	308	5.6	274	1 SUBSD	subtilisin (EC 3.4
13	304.5	5.5	323	2 I39867	microbial serine p
14	299	5.4	326	1 C41335	microbial serine p
15	295	5.3	325	2 JCI085	subtilisin (EC 3.4
16	294	5.3	321	2 JCS460	intracellular alka
17	293.5	5.3	322	2 G83922	intracellular alka
18	289	5.2	319	2 I39866	microbial serine p
19	285.5	5.2	374	2 I39781	subtilisin (EC 3.4
20	284.5	5.1	321	1 S27501	alkaline proteinase
21	283	5.1	380	2 A49778	high-alkaline seri
22	281.5	5.1	1398	2 T28159	pyrolysin (EC 3.4
23	271	4.9	384	2 JCS480	alkaline proteinase
24	270.5	4.9	328	2 G83932	probable protease
25	266	4.8	378	2 A33973	high-alkaline seri
26	260.5	4.7	682	2 S44131	subtilisin-like pr
27	257	4.6	1448	2 A12007	subtilisin family p
28	256	4.6	757	2 C84120	subtilisin-type pr
29	253	4.6	397	2 JH0075	cysteine-dependent

30	251.5	4.5	436	2 I39973	alkaline serine pr
31	250	4.5	442	2 A69587	intracellular alka
32	249.5	4.5	1345	2 T29090	surface layer-asso
33	249	4.5	806	2 A41341	microbial serine p
34	246	4.4	1331	2 A72647	probable surface p
35	243.5	4.4	401	2 A57690	aerolysin precuro
36	243	4.4	645	1 SUBSMP	serine proteinase
37	242	4.4	419	1 S25835	subtilisin (EC 3.4
38	241.5	4.4	412	2 T42024	probable serine pr
39	241.5	4.4	420	1 S23407	subtilisin (EC 3.4
40	241.5	4.4	792	2 H83736	subtilisin-type al
41	240	4.3	401	2 I39974	serine proteinase
42	239	4.3	444	2 B83891	intracellular alka
43	235	4.2	488	2 A11930	proteinase (import
44	231.5	4.2	799	2 G83753	subtilisin-type pr
45	230.5	4.2	361	2 G83756	subtilisin-type al

ALIGNMENTS

RESULT 1					
intraluminal subtilisin-like proteinase Stp, membrane-bound - Chinese hamster					
C:Species: Crictulus griseus (Chinese hamster)					
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004					
C:Accession: T17093					
R:Sakai, J.; Rawson, R.B.; Espanshade, P.J.; Chang, D.; Seegmiller, A.C.; Goldstein, J.					
Molecular Cell 2, 505-514, 1998					
A:Title: Molecular identification of the sterol-regulated luminal protease that cleaves					
A:Reference number: Z18677; PMID:99026600; PMID:9809072					
A:Accession: T17093					
A:Status: preliminary; translated from GB/EMBL/DBJ					
A:Molecule type: mRNA					
A:Residues: 1-1052 <S>					
A:Cross-references: UNIPROT:Q922A8; EMBL:AF078105; NID:G3892203; PID:G3892204; PIDN:AKC					
A:Experimental source: strain 25-RA					
C:Function:					
A:Description: Stp is proposed to be a sterol-regulated protease that controls lipid me					
A>Note: Stp cleaves sterol regulatory element binding proteins (SREBPs) in the ER lumen					
Query Match					
Best local similarity 97.7%; Score 5408; DB 2; Length 1052;					
Matches 1006; Conservative 15; Mismatches 15; Indels 0; Gaps 0;					
QY	1	GKXHLGDRLEKKSFEKAPCPGCSHLTKVRESSVVEYIVAFNGYFTAKARNSFISA	60		
DB	17	GKXHLGDRLEKKSFEKAPCPGCSHLTKVRESSVVEYIVAFNGYFTAKARNSFISA	76		
QY	61	LKSSVDNWRILIPNNPSSDYPDFEYIQEKQKAGLLTLEDPNIRKVTPOKRVFSL	120		
DB	77	LKSSVDNWRILIPNNPSSDYPDFEYIQEKQKAGLLTLEDPNIRKVTPOKRVFSL	136		
QY	121	KYASDPTVPCNETRWQSKQSSRLPRASISLGSFHWATGRSSRLRAIPROVQT	180		
DB	137	KYASDPTVPCNETRWQSKQSSRLPRASISLGSFHWATGRSSRLRAIPROVQT	196		
QY	181	LQADVLQWQGYTGANVAVVDITGLSEKHPFKVKKETNTNERTLDDGAGHGFVAGV	240		
DB	197	LQADVLQWQGYTGANVAVVDITGLSEKHPFKVKKETNTNERTLDDGAGHGFVAGV	256		
QY	241	IASRECGFAPDELHIFRFTNNQVSYTWPLDAFYATILKKIDVNLSTIGGDFMDH	300		
DB	257	IASRECGFAPDELHIFRFTNNQVSYTWPLDAFYATILKKIDVNLSTIGGDFMDH	316		
QY	301	PFVDKVELTANNVIMVSAIGNDGPLYGTINNPDQMDVIGVGIDFEDNIAFSSRGMT	360		
DB	317	PFVDKVELTANNVIMVSAIGNDGPLYGTINNPDQMDVIGVGIDFEDNIAFSSRGMT	376		
QY	361	TWELPGYGRMKPDIIVYAGAVRSGGVKGRALSGTSVAPVAVAGATLLVSTVQREL	420		
DB	377	TWELPGYGRMKPDIIVYAGAVRSGGVKGRALSGTSVAPVAVAGATLLVSTVQREL	436		

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OM protein - protein search, using sw model

Run on: August 17, 2005, 15:18:18 ; Search time 169 Seconds
(without alignments)
2370.910 Million cell updates/sec

Title: US-09-830-837A-6_COPY_17_1052
 Perfect: score: 5537

Sequence: 1 GKKHLDRLKKSFEKAPCP.....PRVKRPQLMQVHPKPTPSV 1036

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Database : A_GeneSeq_16Dec04:*

1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5537	100.0	1052	3	AAB06334	Aab06334 Human sub1
2	5537	100.0	1052	3	AAy54619	Aay54619 Human sub1
3	5537	100.0	1052	3	AAy66982	Aay66982 Human sub1
4	5537	100.0	1052	3	AAy84227	Aay84227 Human sub1
5	5537	100.0	1052	4	AAU38520	Aau38520 Human sub1
6	5537	100.0	1052	5	AAE14527	Aae14527 Human sub1
7	5537	100.0	1052	5	ABG91096	Abg91096 Human sub1
8	5408	97.7	1052	3	AAy84228	Aay84228 Human sub1
9	5408	97.7	1052	5	AAE14528	Aae14528 Human sub1
10	5396	97.5	1052	3	AAAB06335	Aab06335 Human sub1
11	5360	96.8	1052	3	AAAB06336	Aab06336 Human sub1
12	3549	64.1	666	5	ABAB90255	Abab90255 Human sub1
13	2428	43.9	497	7	ADB64193	Adb64193 Human sub1
14	2366.5	42.7	992	4	AAB20015	Aab20015 Human sub1
15	2231	40.3	952	4	AAB63047	Aab63047 Human sub1
16	606	10.6	129	5	ADK34680	Adk34680 Human sub1
17	585	10.9	135	5	ADK36735	Adk36735 Human sub1
18	463	8.4	126	4	AAAO0619	Aao0619 Human sub1
19	343.5	6.2	392	6	ABPS5571	Abps5571 Human sub1
20	340.5	6.1	381	1	AAp60571	Aap60571 Human sub1
21	340.5	6.1	381	1	AAp80744	Aap80744 Human sub1
22	340.5	6.1	381	2	AAp07970	Aap07970 Human sub1
23	338.5	6.1	352	2	AAW46600	Aaw46600 Human sub1
24	338.5	6.1	387	6	ABPS5567	Abps5567 Human sub1
25	338.5	6.1	388	6	ABPS5569	Abps5569 Human sub1

26	338.5	6.1	400.6	ABP59565	Abp59565
27	337.5	6.1	352.2	AAW46595	Amino acid
28	337.5	6.1	381.1	AAEP1060	AAEP1060
29	337.5	6.1	381.2	AAO37377	Wild-type
30	337.5	6.1	381.2	AAAR3411	Subtilisin
31	337.5	6.1	381.2	AAAR4463	AAr24331
32	337.5	6.1	381.2	AAAR4463	Bacillus
33	337.5	6.1	381.2	AAAR4424	AAr74224
34	337.5	6.1	381.2	AAAY9229	B. subtilis
35	336.5	6.1	381.1	AAAP70053	AAy39229
36	336.5	6.1	1079.4	AAAB81180	Bacillus
37	336.5	6.1	1079.6	ABU07391	AAb70053
38	333.5	6.0	275.2	AAAS1928	Transglu
39	332.5	6.0	379.6	AAAZ3994	AAb81180
40	331.5	6.0	381.5	AAAI9063	Abu07391
41	330.5	6.0	275.2	AAAS2643	AAy51928
42	330.5	6.0	275.2	AAAS1924	Bacillus
43	330.5	6.0	275.2	AAAS1929	AAr51924
44	330.5	6.0	275.2	AAAS1920	Bacillus
45	329.5	6.0	275.2	AAAS1927	AAr51920
					Bacillus

ALIGNMENTS

RESULT 1
AAB06334
ID AAB06334 standard; protein; 1052 AA.

AC AAB06334 ;
VV

DT 03-OCT-2000 (first entry)
xx

Human subtilisin-kexin isoenzyme 1.

KW Human; subtilisin-kexin isoenzyme 1; SKI-1; antilipemic; cytostatic;

Ras-dependent cancer; restenosis; amyloid protein formation; KW

steroid-regulatory element-binding protein; SRBEP.

OS Homo sapiens.

PN WO200026348-1

PD 11-MAY-2000.

04-NOV-1999

PR 04-NOV-1998; 98CA-02249648.

PA (RECL-) INST RECH CLINIQUES MONTREAL

PI Seldah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

DR WPI; 2000-365601/31.

XX

PT producing a polypeptide useful for treating hypercholesterolemia, liver

[illegible]

XX
XX
E

The present sequence is human subtilisin-Kexin isoenzyme 1 (SKI-1), a type-1 membrane-bound proteinase. The nucleotide sequence was isolated from the human neuronal cell line IMR-32 by RT-PCR using active site degenerate primers. SKI-1 cleaves at a specific threonine residue within the N-terminal segment of human pro-brain-derived neurotrophic factor (proBDNF). It is also capable of cleaving steroid-regulatory element-binding proteins (SRBPs), which function to control lipid biosynthesis and uptake in animal cells. Peptides which bind to and are cleaved by SKI-1 may be used for monitoring SKI-1 activity, for screening inhibitors of